

FIG. 1

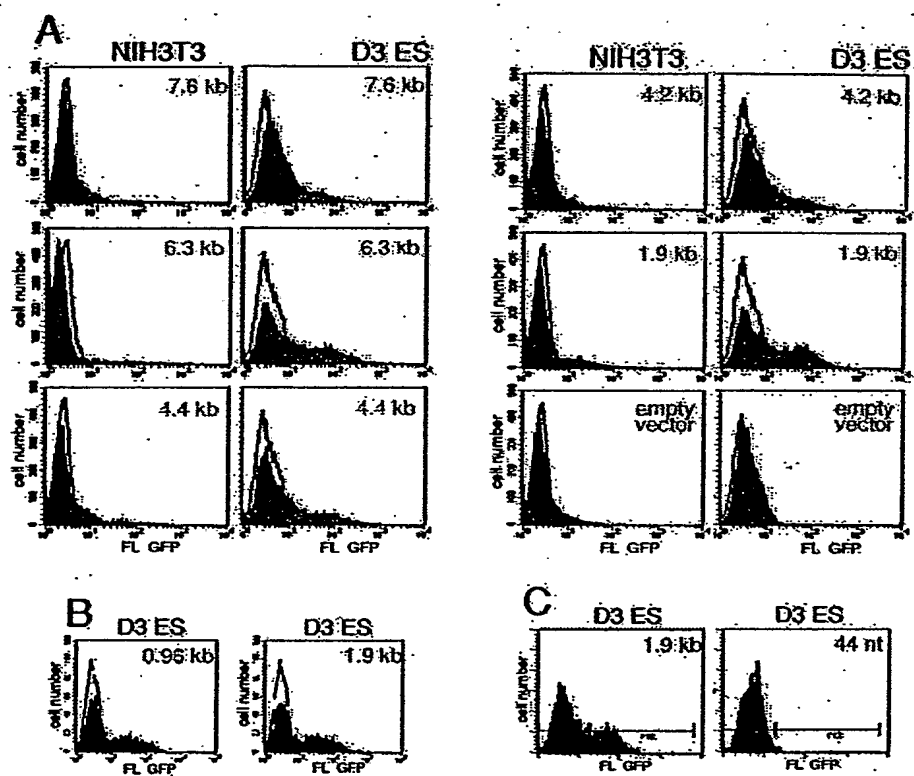


FIG. 2

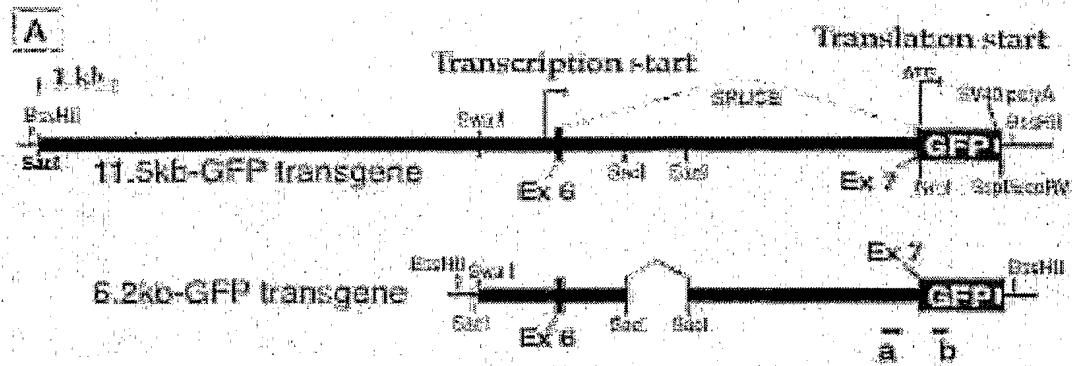


FIG. 3A

TRANSENE COPY NUMBERS

transgene	Lima	# copies
11.5 kb-GFP	A	6
"	C	13
"	D	11
6.2 kb-GFP	Z	17

FIG. 3B

FIG. 4

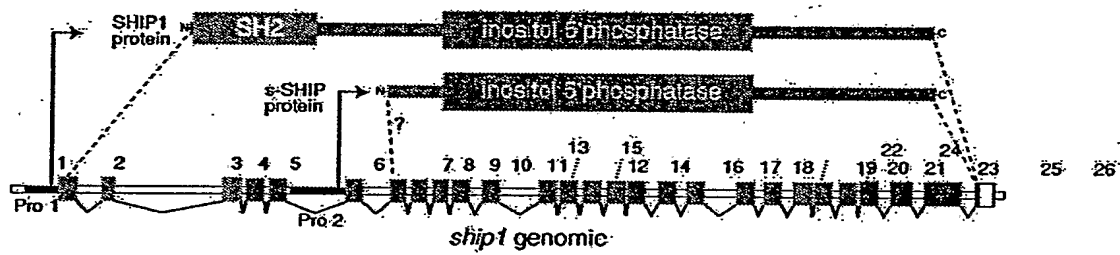


FIG. 5

CLUSTAL W (1.82) multiple sequence alignment

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Hu -----AGCCCAGGATTGGAGTTGTCAATGGATGTGACAATGGGAAAATCCGTCT 50
Mo CTCTGGGTTTCATCAAGAAACCCTACCTCCATAACATAAAGTGTGATGGAGAAAGGCACCT 60

Hu GAGCCTGCATTTGGGCTGCTAGGAGGGGATTGTCAT-CAGA-ATCCACAGATCACCAGCA 108
Mo AATGTCAACCTCAAACCCCTACCTGCATGTGCACACACATACATCCACACCAACACACACA 120

Hu C-TGGGCAGCCCTA---ATATTTAAATGCAGATTCTAGACTCAATCAGGCGGGAGCCCA 164
Mo CACACACACACAC CACACACCACACACACACACACACAAATAAATAAGTAAATAAATAA 180

Hu GAAATTTGCATTTGTTAACACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 224
Mo AATATTTA-GCTCTCCAGACCAAATCTTGGTGAAACCCATGCATTTGCATTTGTGTGTGTGT 239

Hu TTTATAAACACAGAAGGTTGGGAACCATGGA---TAACTAAGTGAAGTCATTTTGTCACT 281
Mo CCTACAAACACTGAAGGTTAAGAAGCATGCTCCTTAGTAATTTTATAGCAGTTTGCCTTT 299

Hu C-AGATTTGAATT---TTCTACAGGCTATAGAGTGCAGTTTGGCTAAAGCAAAACCTAGG 337
Mo CCAGATTGAAAACAGATTCTATAGGCTACACAGTGCTAAATGGATTATGC-----TCAGA 354

Hu TACAGTCAGGACTACACAATTCAGTTTCGCTGTGGGTTGGGAAGGGATGGGTGGGGCCAGT 397
Mo TACAGATTGAAAAGGATA---CAGATTGAAAAGGGTCCGGG-----GTCTGGGGCCAG- 402

Hu GCTGGCAAGCCT-TGATCTTTGCCCGGGCTTGTCCTTCTGGGGAGAAATTACCTGCTTCTG 456
Mo GATGACGGGCCAACTATCTTTGCCCGGGCTTGTCCTTCAGGGAAGGGTTACAGGATTCAC 462

Hu CTGGACTGAGG-GTGCCCTCATCTCTGGCTAGAGCCCGTGCTGCCATGGAAGACTCTTTC 515
Mo C---ACTGGGGTGTGGCCT-ATCTGCTGTAGGACCTGAATTGCC-TGGAG---TGTTTC 514

Hu CGGTGCCCACTAATCCTTGATGTTACCTTGT-CCCCTGCCCCCAG 560
Mo TAGTTCCCACTAGTTGTTGAACCTTACCTTGAACCTCTGCTCCCAG 560

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FIG. 6

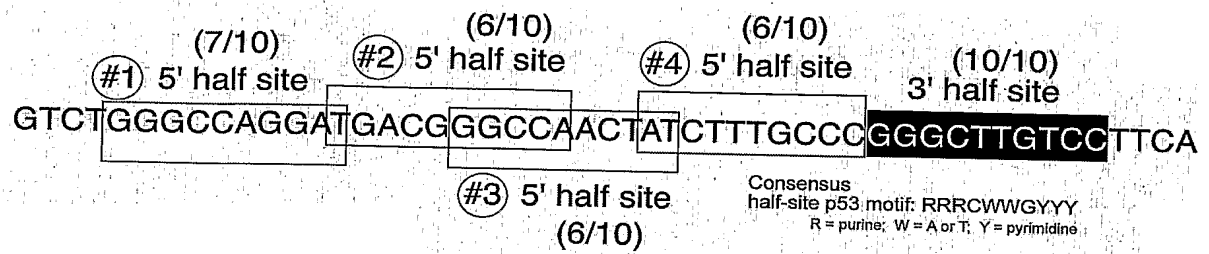


FIG. 7